

## Sarah N Anderson

Department of Plant and Microbial Biology  
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### EDUCATION

2016 Ph.D. Integrative Genetics and Genomics. University of California, Davis.

2011 B.S. Genetics, Magna Cum Laude with Honors. Iowa State University.

### RESEARCH EXPERIENCE

2016 – present Postdoctoral associate at the University of Minnesota, Twin Cities.  
Advisor: Nathan Springer, Department of Plant and Microbial Biology

2012 – 2016 Graduate student researcher at the University of California, Davis. Advisor:  
Venkatesan Sundaresan, Department of Plant Biology. Dissertation: Maternal to Zygotic  
Transition in *Oryza sativa*.

2009 – 2011 Undergraduate research assistant at Iowa State University. Advisor: Yanhai Yin,  
Department of Genetics, Development and Cell Biology. Honors Thesis: Identification of  
signaling components in the control of plant growth by activation tagging with *herk1 the1*  
mutant in *Arabidopsis*.

### PUBLICATIONS

2019 **SN Anderson**, MC Stitzer, P Zhou, JM Noshay, J Ross-Ibarra, CD Hirsch, NM Springer.  
Dynamic patterns of transcript abundance of transposable element families in maize.  
*BioRxiv*. <https://doi.org/10.1101/668558>. (Preprint)

2019 **SN Anderson**, MC Stitzer, AB Brohammer, P Zhou, JM Noshay, CD Hirsch, J Ross-  
Ibarra, CN Hirsch, NM Springer. Transposable elements contribute to dynamic genome  
content in maize. *BioRxiv*. <https://doi.org/10.1101/547398>. (Preprint)

2019 MC Stitzer, **SN Anderson**, NM Springer, J Ross-Ibarra. The genomic ecosystem of  
transposable elements in maize. *BioRxiv*. <https://doi.org/10.1101/559922>. (Preprint)

2019 W Xue, **SN Anderson**, X Wang, L Yang, PA Crisp, Q Li, JM Noshay, PS Albert, JA  
Birchler, P Bilinski, MC Stitzer, J Ross-Ibarra, S Flint-Garcia, X Chen, NM Springer, JF  
Doebley. Hybrid decay: a transgenerational epigenetic decline in vigor and viability  
triggered in backcross populations of teosinte with maize. *BioRxiv*.  
<https://doi.org/10.1101/588715>. (Preprint)

- 2019 PA Crisp, JM Noshay, **SN Anderson**, NM Springer. Opportunities to use DNA methylation to distil functional elements in large crop genomes. *Molecular Plant*. <https://doi.org/10.1016/j.molp.2019.02.006>.
- 2018 NM Springer, **SN Anderson**, CM Andorf, KR Ahern, F Bai, O Barad, WB Barbazuk, HW Bass, K Baruch, G Ben-Zvi, ES Buckler, R Bukowski, MS Campbell, EKS Cannon, P Chomet, RK Dawe, R Davenport, HK Dooner, LH Du, C Du, KA Easterling, C Gault, JC Guan, CT Hunter, G Jander, Y Jiao, KE Koch, G Kol, TG Köllner, T Kudo, Q Li, F Lu, D Mayfield-Jones, W Mei, DR McCarty, JM Noshay, JL Portwood, G Ronen, AM Settles, D Shem-Tov, J Shi, I Soifer, JC Stein, MC Stitzer, M Suzuki, DL Vera, E Vollbrecht, JT Vrebalov, D Ware, S Wei, K Wimalanathan, MR Woodhouse, W Xiong, TP Brutnell. The maize W22 genome provides a foundation for functional genomics and transposon biology. *Nature Genetics* 50, 1282-1288.
- 2018 **SN Anderson**, G Zynda, J Song, Z Han, M Vaughn, Q Li, NM Springer. Subtle perturbations of the maize methylome reveal genes and transposons silenced by chromomethylase or RNA-directed DNA methylation pathways. *G3: Genes, Genomes, Genetics* 8(6), 1921-1932.
- 2018 C Johnson, LJ Conrad, R Patel, **SN Anderson**, C Li, A Pereira, V Sundaresan. Reproductive lincRNAs in rice consist of male gamete specific and PRC2- repressed classes. *Plant Physiology* pp.01269.2017.
- 2018 **SN Anderson**, NM Springer. Potential roles for transposable elements in creating imprinted expression. *Current Opinion in Genetics & Development* 49, 8-14.
- 2017 **SN Anderson**, C Johnson, J Chesnut, DS Jones, I Khanday, M Woodhouse, C Li, LJ Conrad, S Russell, V Sundaresan. The zygotic transition is initiated in unicellular plant zygotes with asymmetric activation of parental genomes. *Developmental Cell* 43 (3), 349-358.
- 2017 SD Russell, DS Jones, **SN Anderson**, X Wang, V Sundaresan, X Gou. Isolation of rice sperm cells for transcriptional profiling. *Plant Germline Development*, 211-219.
- 2017 R Oka, J Zicola, B Weber, **SN Anderson**, C Hodgman, JI Gent, J Wesslink, NM Springer, HCJ Hoefsloot, F Turck, M Stam. Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize. *Genome Biology* 18(1):137.
- 2013 **SN Anderson**, C Johnson, D Jones, LJ Conrad, X Gou, S Russell, V Sundaresan. Transcriptomes of isolated rice gametes characterized by deep sequencing: Evidence for distinct sex-dependent chromatin and epigenetic states before fertilization. *The Plant Journal* (Cover article) 76(5):729-41.
- 2011 X Yu, L Li, J Zola, M Aluru, H Ye, A Foudree, H Guo, **SN Anderson**, S Aluru, P Liu, S Rodermeil, Y Yin. A Brassinosteroid transcriptional network revealed by genome-wide identification of BES1 target genes in *Arabidopsis thaliana*. *The Plant Journal* 65(4):634-646.

## ORAL PRESENTATIONS

- 2019 “Transposable element contributions to the dynamic genome and transcriptome in maize.” Invited talk at the Danforth Plant Sciences Center in St. Louis, MO.
- 2018 “Transposable element contributions to the dynamic maize genome and transcriptome.” 60<sup>th</sup> Annual Maize Genetics Conference. St. Malo, France.
- 2017 “Analysis of transposon expression provides insights into TE-genome conflicts in maize.” MPGI Fall Symposium: Genomics of Conflict. University of Minnesota. St. Paul, MN.
- 2017 “Dynamic transposable element expression across development in maize.” Plant and Animal Genomes conference; Transposon Workshop. San Diego, CA.
- 2017 “Initiation of zygotic genome activation in the unicellular rice zygote.” Plant and Animal Genomes conference; NuGen Workshop. San Diego, CA.
- 2015 “Transcriptome analysis of the plant zygotic transition reveals differential contributions of parental genomes.” NAIST Biology Workshop. Osaka, Japan.
- 2015 “Transcriptome analysis of the plant zygotic transition reveals differential contributions of parental genomes.” 13<sup>th</sup> International Symposium on Rice Functional Genomics. Wuhan, China.
- 2015 “Transcriptome analysis of the plant zygotic transition.” Invited talk at Shanxi University in Taiyuan, China.
- 2013 “Expression of epigenetic regulators in rice gametes suggests dynamic changes during plant fertilization.” 11th International Symposium on Rice Functional Genomics. New Delhi, India.

## POSTER PRESENTATIONS

- 2019 “Transposable element contributions to maize genome variation”. 61<sup>st</sup> Annual Maize Genetics Conference. St. Louis, MO.
- 2018 “Transposable element contributions to structural and epigenomic variation among maize genomes”. Meeting on Transposable Elements. Cold Spring Harbor, NY.
- 2017 “Dynamic transposable element expression across development and stress in maize.” 59<sup>th</sup> Annual Maize Genetics Conference. St. Louis, MO.
- 2016 “The rice zygote transcriptome reveals early initiation of the maternal to zygotic transition and partial activation of the paternal genome before the first zygotic cell division.” 58<sup>th</sup> Annual Maize Genetics Conference. Jacksonville, FL.
- 2015 “The maternal to zygotic transition in plants occurs before the first zygotic division.” Society for Developmental Biology West Coast Meeting. Yosemite, CA.
- 2014 “Investigating the timing and regulation of the maternal to zygotic transition in plants through the study of gamete and zygote transcriptomes of *Oryza sativa*.” 12th International Symposium on Rice Functional Genomics. Tucson, AZ.

2012 “Genomics of the maternal to zygotic transition in rice.” 54<sup>th</sup> Annual Maize Genetics Conference. Portland, OR.

### **AWARDS AND HONORS**

2018 University of Minnesota MPGI travel grant  
2017 University of Minnesota Postdoctoral Associate Career Development Award  
2017 Department of Plant and Microbial Biology Poster Award  
2016 Integrative Genetics and Genomics Academic Excellence Award  
2015 UC Davis Graduate Student Travel Award  
2015 Henry A. Jastro Graduate Research Scholarship Award  
2014 Outstanding Poster Award, International Symposium on Rice Functional Genomics  
2014 Best Student Poster, Integrative Genetics and Genomics Graduate Group Colloquium  
2014 Elise Stocking Memorial Fellowship  
2013 Honorable Mention, NSF Graduate Research Fellowship Program  
2012 Best Student Poster, Genetics Graduate Group Colloquium  
2012 Honorable Mention, NSF Graduate Research Fellowship Program

### **ACADEMIC SERVICE**

2019 University of Minnesota undergraduate research symposium judge  
2015 – 2016 Integrative genetics and genomics graduate group student chair  
2016 Integrative genetics and genomics colloquium planning committee student chair  
2014 – 2015 Integrative genetics and genomics graduate group admissions committee  
2012 – 2014 Genetics graduate group recruitment committee

Served as reviewer: Bioinformatics, Current Biology, Gene, International Journal of Molecular Sciences, Nature Communications, Nature Plants, PNAS

### **TEACHING EXPERIENCE**

2019 Guest lecturer on molecular markers and gene mapping: Introduction to genetics, University of Minnesota. Instructor: Nathan Springer. April 2019.

2017 Guest lecturer on transposable elements: Plant genomics, University of Minnesota. Instructor: Cory Hirsch. September 2017.

2017 Guest lecturer on plant reproduction: Introduction to genetics, University of Minnesota. Instructor: Nathan Springer. February 2017.

2015 Teaching assistant: Principals of genetics laboratory, University of California, Davis. Instructors: JoAnne Engebrecht and Venkatesan Sundaresan.

2014 Guest lecturer on gametophyte genetics: Plant biology graduate group core course series, University of California, Davis. Instructor: Luca Comai.

2012 – 2014 Instructor, University of Oklahoma-University of California Davis Summer Internship Program in Plant Molecular Biology.

2013 Teaching assistant: Introductory genetics, University of California, Davis. Instructors: Michael Turelli and Chuck Langley.

**TRAINING**

Undergraduate assistants: Dominick Tucker (2015-2016), Jonathan Giesler (2016-2017), Paradis Vandeputte (2017-2018).